

Book Review

SNEATH, P. H. A. and SOKAL, R. R., 1973. Numerical Taxonomy. The principles and practice of numerical classification. W. H. Freeman and Co., San Francisco. Hard covers, xv + 573 pages, 81 diagrams and nine tables within the text. Two appendices, 1641 references, author and subject index. Size: 6¾ x 10 inches; Price: U.S. \$19.50.

One objective of students of systematics is to determine the phylogenetic relationships of various groups of organisms, living or extinct, using every means available. A second objective is to perceive patterns of relationships among these groups of organisms (taxa), and to formalize these patterns into a system of classification. There are several active schools of procedure, each defending its position and methodology. The numerical taxonomy school is one of the most active and revolutionary of these. Its popularity undoubtedly results from rapid advancements in the field of computer and electronic data processing occurring during recent years, and from the increasing availability of these techniques to systematists.

Sneath and Sokal's book is not just a revised edition of their 1963 treatise on the subject, but it is a completely new and comprehensive review of numerical taxonomy, its principles, practice and application to biosystematics. The scope of the book has been broadened considerably and discussion encompasses a much wider range of numerical taxonomy applications, including ecology, biogeography, medicine, social sciences, etc., than the first edition.

The book is organized into twelve chapters (number of pages for each is indicated in brackets): aims and principles of numerical taxonomy (15); taxonomic principles (52); estimation of taxonomic resemblance (74); taxonomic structure (121); study of phylogeny (53); population phenetics (19); identification and discrimination (28); implications for nomenclature (8); critical examination of numerical taxonomy (26); numerical taxonomy in fields other than biological systematics (16); and the future of systematics (3).

The book is not exactly bed time reading for the uninitiated. Readers are expected to have a basic knowledge of statistics, matrix algebra, elementary set and graph theory, etc. if they are to follow the theory and implications of numerical taxonomy set forth in the book. The text is supplemented by graphs and diagrams where appropriate, but the readers not well versed in mathematics may have difficulty understanding some of the equations.

The diagrams are clear, well labelled and illustrative. An extensive, cross-referenced subject index is invaluable and makes this highly complex book easier to use. The text is remarkably free of typographical errors and the book is very clearly written.

Practitioners and proponents of numerical taxonomy assert that phylogenetic relationships among taxa cannot be determined accurately and that classifications based upon such relationships are distorted to the degree of uselessness. Also, they claim repeatedly that taxonomy will not become a science until its basic units are quantified and precisely defined. These objections are supposedly eliminated by numerical taxonomy, a system that can be conveniently devised through statistical analysis in evaluating the structure (phenotype) of the subjects to be classified. The same system can be applied also to the classification of pebbles or other non-biological objects.

The underlying basic tenet of numerical taxonomic philosophy (although nowhere explicitly stated in the book) seems to be that the phenotype is a direct evolutionary byproduct and thus organisms closely related phylogenetically are more similar to each other than to other organisms, *c.f.* (p. 53): "The theoretical principle of descent with modifications - phylogenetics - is clearly responsible for the existence and structure of a natural system of classification; (p. 422): Yet this discovery must be based on phenetic evidence; (p. 56): Thus, when told that a new species of the genus *Rana* has been described, we can immediately make many predictions about its appearance, without ever having seen it. This follows from the naturalness of the genus *Rana*,

in the sense in which we use the concept in this book." The hypothesis of correlation between similarity of organisms and their relatedness phylogenetically has to be proven yet, but even the initial selection of subjects to be analysed with techniques of numerical taxonomy presupposes it. For example, one does not select his study subjects at random, from among, for example, trematodes, fishes, insects, etc. to produce a classification: instead a selected group of supposedly related organisms is studied to evaluate their phenotypic variation and to produce a classification based upon it.

Similarity and taxonomic relationship are measured as statistical averages, or compounded similarities (dissimilarities), in characters chosen from the entities to be classified, and are referred to as *operational taxonomic units* (OTU's). OTU's can therefore differ in rank, e.g. they may be individuals, species or higher taxa. The OTU is, for analytical purposes, substituted for by a matrix of characters derived from it, e.g. in the case of an individual, by a set of parameters which best circumscribe its nature. The unit character is defined as "a taxonomic character of two or more states, which within the study at hand cannot be subdivided logically, except for subdivisions brought about by the method of coding." Since the matrix is only a substitute for the real OTU, the more characters that are used, the better substitute this matrix will be. Note the difference between matrices produced for discrimination of taxa, where only a limited number of selected characters is needed. The actual computations used in measuring resemblance vary, and there is no single numerical taxonomic method. Resemblance is usually expressed by coefficients of similarity or dissimilarity and the coefficients are tabulated, again in matrix form, with one coefficient for every pair of OTU's. The taxa are subsequently constructed through cluster analysis, a technique designed to disclose the structure of the similarity matrix, and are often represented in graphic form as a dendrogram or a contour diagram.

The implications of numerical taxonomy for systematics in general are discussed in Chapters 6-12. Major topics are numerical approaches to the study of phylogeny (cladistics), phenetic study of populations, implications of numerical taxonomy for discrimination and identification of taxa (keys). Chapter 9, Implications for nomenclature, is interesting as it discusses many aspects of taxonomic nomenclature. However, the arguments presented, suggesting that the Linnaean system of nomenclature is to be replaced by some other system, remain unsupported.

The weaknesses of numerical taxonomic philosophy and methods are critically reviewed in Chapter 10. The theory, concepts, assumptions and limitations of numerical taxonomy, discussed in previous chapters together with this final recapitulation present an up-to-date theoretical basis for numerical taxonomy. The brief concluding chapter touches upon various developments in other fields which might affect the future practice of taxonomy. How many of them will be realized only time can tell.

Two appendices are provided. Appendix A is a list of publications reporting the use of numerical analyses, arranged alphabetically by author under major headings, e.g. Studies of Arthropoda. Appendix B, Some hints on techniques, sources, and references, is just that and will be appreciated by the neophyte. The bibliography provides ample entry into the voluminous literature.

This is a highly recommended book for any taxonomist, and the best account of numerical taxonomy available.

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